

ASAP Web results

date:2023-02-14T10:21:42
input file:Stictochironomus-Alignment-3.fas
nb of sequences:704
length of seqs:658
subst. model:K80 Kimura
recurs split pval:1.000000e-02

Split probability: 0.010000 sequence length: 658

Save Spart text File [here](#)

Save Spart XML File [here](#)

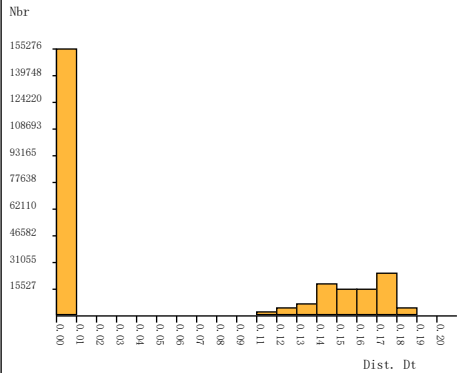
10 best partitions found by ASAP (see [FAQ](#) for more details)

The lower the score, the better the partition

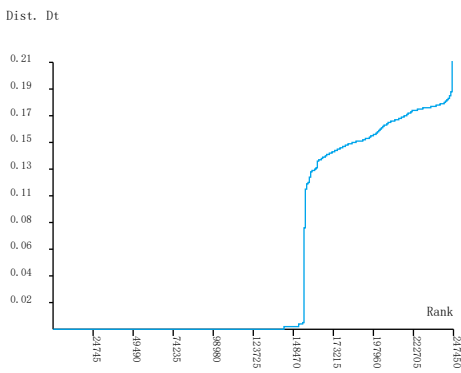
Nb of subsets	asap-score		P-val (rank)	W (rank)	Treshold dist.	Text
* 26	2.50	●	8.55e-03 (2)	9.71e-04 (3)	0.048527	list csv
* 27	3.50	●	2.46e-02 (5)	1.87e-03 (2)	0.026290	list csv
24	4.50	●	2.01e-02 (4)	7.64e-05 (5)	0.069020	list csv
22	8.50	●	1.70e-02 (3)	6.09e-05 (14)	0.073653	list csv
* 45	10.50	●	4.79e-02 (9)	6.27e-05 (12)	0.006204	list csv
19	10.50	●	6.32e-02 (11)	6.55e-05 (10)	0.088886	list csv
26	12.00	●	2.26e-01 (20)	2.16e-04 (4)	0.056231	list csv
* 38	17.00	●	2.57e-02 (6)	2.63e-05 (28)	0.009415	list csv
13	18.50	●	1.00e-05 (1)	7.11e-06 (36)	0.104006	list csv
15	20.50	●	4.01e-02 (8)	1.83e-05 (33)	0.101450	list csv

Number of subsets in this table equals to the number of primary species hypotheses in the respective partition

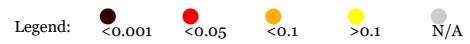
Histogram of distances [\[save\]](#)



Ranked distances [\[save\]](#)



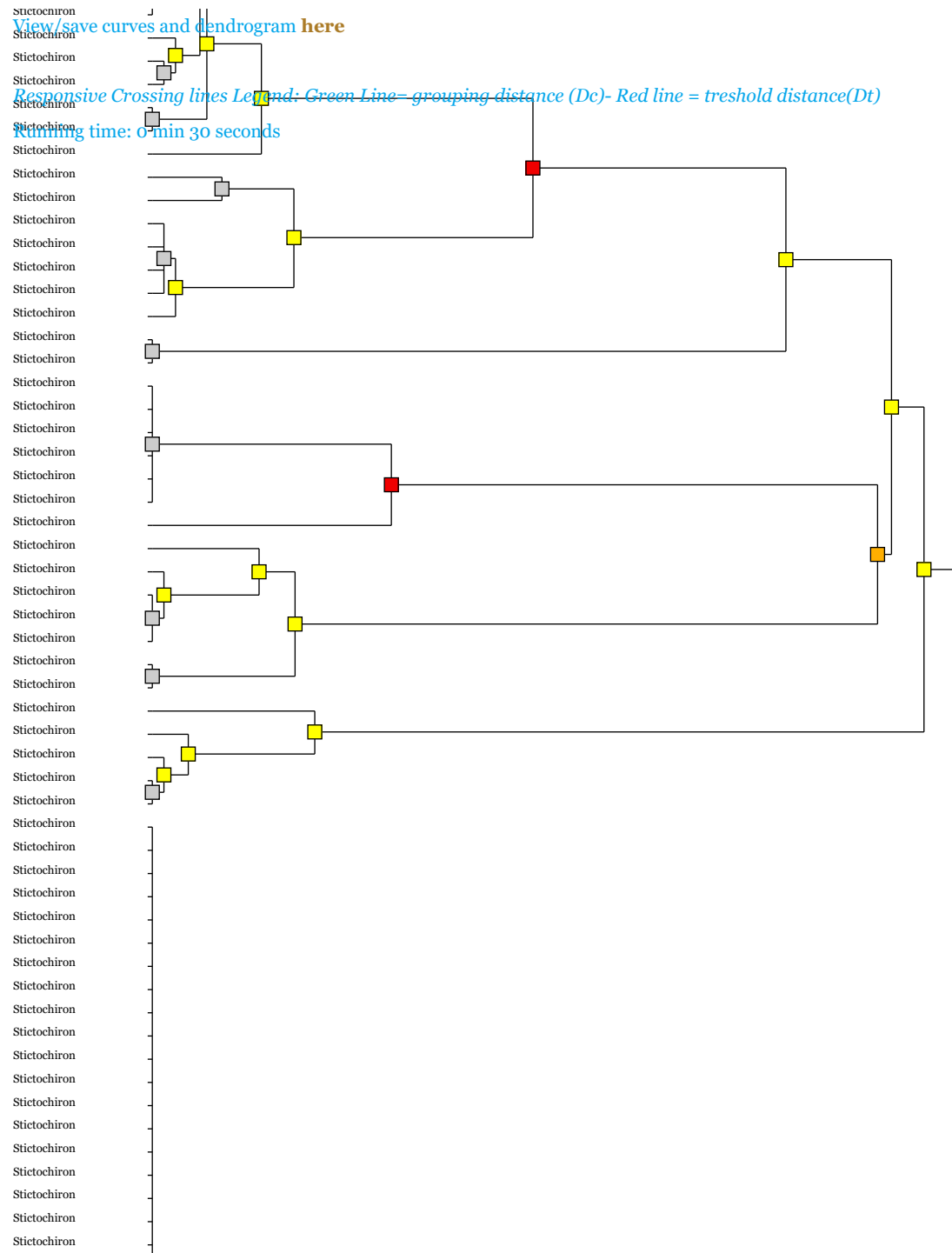
[View/Save Boxed subsets graph here](#)



View/save curves and dendrogram [here](#)

Responsive Crossing lines Legend: Green Line= grouping distance (Dc)- Red line = threshold distance(Dt)

Running time: 0 min 30 seconds



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The dendrogram illustrates the hierarchical clustering of 40 *Stictochiron* samples. The tree structure is highly branched, indicating low similarity between most samples. Three specific clusters are highlighted with colored squares: a grey square at the bottom left, a dark red square in the middle right, and a yellow square at the bottom right. The x-axis represents distance, with a scale from 0 to 100.

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[illegible]

